

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 27, 2004, 21:39:31 ; Search time 21 Seconds
(without alignments)
501.509 Million cell updates/sec

Title: US-10-633-202-2_COPY_399_602
Perfect score: 1192
Sequence: 1 PYPGNIPLKYCGNLVVEEG.....QFHLNDTTCWGTDYHLGMAI 204

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	864	72.5	722	4	US-09-617-145-2
2	431.5	36.2	751	2	US-08-836-443-3
3	422.5	35.4	787	4	US-09-548-797B-5
4	422.5	35.4	802	4	US-09-632-098-2
5	422.5	35.4	812	4	US-09-632-098-4
6	422.5	35.4	849	4	US-09-548-797B-6
7	401.5	33.7	814	3	US-09-813-819-4
8	401.5	33.7	814	4	US-09-920-048-4
9	401.5	33.7	855	3	US-09-813-819-2
10	390	32.7	651	1	US-08-264-101-2
11	390	32.7	651	2	US-08-765-243-2
12	390	32.7	651	5	PCT-US95-07295-2
13	390	32.7	734	2	US-08-765-243-8
14	390	32.7	734	5	PCT-US95-07295-8
15	384.5	32.3	696	3	US-09-351-414-2
16	384	32.2	670	1	US-08-243-542-3
17	384	32.2	670	1	US-08-477-407-3
18	384	32.2	670	1	US-08-484-355-3
19	384	32.2	769	1	US-08-243-542-4
20	384	32.2	769	1	US-08-477-407-4
21	384	32.2	769	1	US-08-484-355-4
22	384	32.2	769	1	US-08-786-256C-15
23	368	30.9	775	4	US-09-786-256C-32
24	368	30.9	775	4	US-08-264-101-4
25	359	30.1	457	1	US-08-765-243-4
26	359	30.1	457	1	US-08-765-243-4
27	359	30.1	457	5	PCT-US95-07295-4

28	359	30.1	735	2	US-08-765-243-6
29	359	30.1	735	5	PCT-US95-07295-6
30	347	29.1	524	1	US-08-243-542-2
31	347	29.1	524	1	US-08-477-407-2
32	347	29.1	524	1	US-08-484-355-2
33	345	28.9	746	4	US-09-548-797B-4
34	344	28.9	488	1	US-08-243-542-1
35	344	28.9	488	1	US-08-477-407-1
36	344	28.9	488	1	US-08-484-355-1
37	342.5	28.7	781	4	US-09-738-946-8
38	332.5	27.9	616	4	US-09-608-790-1
39	312	26.2	613	4	US-09-026-001A-10
40	312	26.2	621	4	US-09-026-001A-18
41	306.5	25.7	621	4	US-09-026-001A-6
42	283.5	23.8	540	4	US-09-786-256C-1
43	283.5	23.8	540	4	US-09-786-256C-30
44	272	22.8	529	2	US-08-836-442-3
45	270.5	22.7	462	4	US-09-026-001A-16

ALIGNMENTS

RESULT 1

US-09-617-145-2
; Sequence 2, Application US/09617145
; Patent No. 6485956
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas P.
; TITLE OF INVENTION: SVPH1-8 DNA and Polypeptides
; FILE REFERENCE: 03260.0050-00304
; CURRENT APPLICATION NUMBER: US/09/617,145
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/071,505
; PRIOR FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-617-145-2

Query Match	72.5%	Score	864	DB	4	Length	722
Best Local Similarity	70.6%	Pred. No.	1.2e-63				
Matches	144	Conservative	24	Mismatches	36	Indels	0
Gaps	0						
Qy	1	PYPGNIPLKYCGNLVVEEGECDCGTIRQCAKDPCCLLNCTLRPGACAFGLCKCKCF	60				
Db	398	PRLGEIFMLKRCGNGWVERBQDCGSCVQCEQDACLLNCTLRPGACAFGLCKCKCF	457				
Qy	61	LPSGTLCRQVGECDLPWCNGTSHQCDDVYVQDGISCNVNAFCYEKTCNNHDIQCKEI	120				
Db	458	MPSGELCQFVNECDLPWCNGTSHQCDDVYVQDGIPCSDSAYCYKRCNNHQCREI	517				
Qy	121	FGDARSASQCYQBINTQGNRFGHCGIVGTYVVKWTPDIMGCRVQCNVGVIPNLIEH	180				
Db	518	FGDAKASQNCYKEINSQGNRFGHCGINGITTLKCHISDVFCGRVQCNVNDIPLLQDH	577				
Qy	181	STVQOFHLNDTTCWGTDYHLGMAI	204				
Db	578	FTLQTHINGVTCWGIDYHLRMI	601				
RESULT 2							
US-08-836-443-3							
; Sequence 3, Application US/08836443							
; Patent No. 5883241							
; GENERAL INFORMATION:							
; APPLICANT: DOCHERTY, Andrew, J.P							
; APPLICANT: SLOCOMBE, Patrick, M.							
; TITLE OF INVENTION: DNA SEQUENCES CODING FOR A							
; TITLE OF INVENTION: HUMAN METALLOPROTEINASE AND VARIANTS THEREOF							

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 27, 2004, 21:28:15 ; Search time 128 Seconds
(without alignments)
450.310 Million cell updates/sec

Title: US-10-633-202-2_COPY_399_602

Perfect score: 1192

Sequence: 1 PYPGNIFRLKYGNIWVEG.....QPHLNDTTCWGTDYHLGMAI 204

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1192	100.0	726	2	AAY17413 Human SVP
2	1192	100.0	726	2	AAY03223 Amino aci
3	1192	100.0	726	7	Adc78877 Human PRO
4	1192	100.0	776	6	Abr39425 Human GEN
5	1128	94.6	535	2	AAY17414 SVPH1-26
6	1128	94.6	535	4	Aae13056 ADAM-20di
7	864	72.5	542	2	AAY03224 Amino aci
8	864	72.5	722	2	AAY28655 Human SVP
9	864	72.5	722	6	Abg76200 Human sna
10	840	70.5	523	4	Aae13057 ADAM-21di
11	788	66.1	766	3	Aab07739 A snake v
12	788	66.1	787	3	Aab07740 A snake v
13	788	66.1	820	3	Aab07741 A snake v
14	773	64.8	528	4	Aae13061 ADAM-29di
15	590.5	49.5	499	3	Aab07738 A snake v
16	590.5	49.5	781	3	Aab07743 A snake v
17	590.5	49.5	790	3	Aab07742 A snake v
18	590.5	49.5	790	3	Aab07705 Amino aci
19	590.5	49.5	790	4	Aau12273 Human PRO
20	590.5	49.5	790	6	Abol17717 Novel hum
21	590.5	49.5	790	6	Abu80971 Human PRO
22	590.5	49.5	790	6	Abu66671 Human PRO
23	590.5	49.5	790	6	Abu59752 Novel sec
24	590.5	49.5	790	6	Abu24942 Human sec
25	590.5	49.5	790	6	Abu66947 Human sec

ALIGNMENTS

RESULT 1

AAY17413
ID AAY17413 standard; protein; 726 AA.
XX
AC AAY17413;
XX
DT 26-JUL-1999 (first entry)
XX
XX Human SVPH1-26 protein.
DE
XX
XX Human; SVPH1-26; proteinase; testis; fertilisation; spermatogenesis;
KW birth control; detergent additive; diagnosis; testicular cancer.
XX
OS Homo sapiens.
XX
XX WO9923228-A1.
XX
PD 14-MAY-1999.
XX
XX 30-OCT-1998; 98WO-US022965.
XX
XX 30-OCT-1997; 97US-0063571P.
XX
(IMMV) IMMUNEX CORP.
PI Cerretti DP;
XX
XX WPI; 1999-337487/28.
DR N-PSDB; AAX56461.
XX
XX New human SVPH1-26 DNA useful for the diagnosis and prognosis of testicular cancers.
XX
XX Claim 2; Page 73-83; 96pp; English.

The present sequence is human SVPH1-26. Human SVPH1-26 polypeptides are proteinases implicated in fertilisation and spermatogenesis. They can be used as therapeutic agents. A proteinase inhibitor of the catalytic domain would inhibit SVPH1-26 activity and would be useful as a method for birth control. Also, an inhibitor of the disintegrin domain of SVPH1-26 may affect fertilisation. The proteinase activity of SVPH1-26 can also be used as a detergent additive for the removal of stains having a protein component. The SVPH1-26 polypeptides and fragments can also be used as molecular weight markers, as markers for determination of isoelectric points of sample proteins and as controls for establishing the extent of fragmentation of a protein sample. The products can also be used for identifying, separating or purifying cells that express SVPH1-26 polypeptides such as testis cells. They can be used for the diagnosis and

26 590.5 49.5 790 6 ADA45723 Novel hum
27 590.5 49.5 790 6 ADA76154 Human PRO
28 590.5 49.5 790 6 ADA18804 Human PRO
29 590.5 49.5 790 6 ADA61427 Homo eapi
30 590.5 49.5 790 6 ADB19212 Novel hum
31 590.5 49.5 790 6 ADB27753 Human PRO
32 590.5 49.5 790 6 ADA86232 Novel hum
33 590.5 49.5 790 6 ADA86232 Novel hum
34 590.5 49.5 790 6 ADA47582 Human PRO
35 590.5 49.5 790 6 ADA67377 Human PRO
36 590.5 49.5 790 6 ADB30384 Human PRO
37 590.5 49.5 790 6 ADA85680 Novel hum
38 590.5 49.5 790 6 ADA96892 Human PRO
39 590.5 49.5 790 6 ADA79196 Human PRO
40 590.5 49.5 790 6 ADA87335 Novel hum
41 590.5 49.5 790 6 ADB16537 Human PRO
42 590.5 49.5 790 6 ADA91629 Novel hum
43 590.5 49.5 790 6 ADB14692 Human PRO
44 590.5 49.5 790 6 ADB18653 Novel hum
45 590.5 49.5 790 6 ADA93868 Human PRO

```
CC prognosis of testicular cancers
SQ Sequence 726 AA;
Query Match 100.0%; Score 1192; DB 2; Length 726;
Best Local Similarity 100.0%; Pred. No. 8.4e-88;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PYPGNIFRLKYCGNLVVEEGECDCGTIRQCAKDPCCLLNCTLHPGAACAFGICCKDKCF 60
Db 399 PYPGNIFRLKYCGNLVVEEGECDCGTIRQCAKDPCCLLNCTLHPGAACAFGICCKDKCF 458
QY 61 LPSGTLCRQOVGECDLPEWNCSTSHQCPDDVVVDGISCNVNAFCYEKTCNNHDIQCKEI 120
Db 459 LPSGTLCRQOVGECDLPEWNCSTSHQCPDDVVVDGISCNVNAFCYEKTCNNHDIQCKEI 518
QY 121 FQDARSASQSCYQBIINTQGNRFGHCGIVGTTVVKWTPDIMCGRVQCNVGVIPNLIEH 180
Db 519 FQDARSASQSCYQBIINTQGNRFGHCGIVGTTVVKWTPDIMCGRVQCNVGVIPNLIEH 578
QY 181 STVQOFHLNDTTCWGTDYHLGMAI 204
Db 579 STVQOFHLNDTTCWGTDYHLGMAI 602
RESULT 2
AAY03223
ID AAY03223 standard; protein; 726 AA.
XX AC AAY03223;
XX DT 16-AUG-1999 (first entry)
XX DE Amino acid sequence of the novel metalloprotease ADAM 16a.
XX KW membrane metalloprotease protein; human; ADAM 16a; testis; contraceptive;
XX KV vaccine; fertility diagnosis; fertility treatment.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Peptide 1..31
FT Protein /note= "signal peptide"
FT FT 32..727
FT FT /note= "mature protein"
XX WO9907856-A1.
XX PD 18-FEB-1999.
XX PF 05-AUG-1998; 98WO-EP004859.
XX PR 07-AUG-1997; 97GB-00016755.
XX PA (GLAX ) GLAXO GROUP LTD.
XX PI Hooft Van Huijsduinen RAM;
XX WPI; 1999-190050/16.
XX DR N-PSDB; AAX28636.
XX New metalloprotease proteins ADAM16a and ADAM16b - useful in
XX contraception, and in the evaluation and treatment of fertility.
XX Claim 1; Fig 3A; 59pp; English.
XX This is a amino acid sequence of the novel membrane metalloprotease
XX protein designated ADAM 16a, isolated from human testis, and used in the
XX method of the invention. It may be used in contraceptive, vaccines, or in
XX fertility diagnosis and treatment. It may be involved sperm maturation,
XX or fertilisation through mechanisms such as proteolysis, cell adhesion,
XX cell fusion, or intracellular signalling
XX
```

```
SQ Sequence 726 AA;
Query Match 100.0%; Score 1192; DB 2; Length 726;
Best Local Similarity 100.0%; Pred. No. 8.4e-88;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PYPGNIFRLKYCGNLVVEEGECDCGTIRQCAKDPCCLLNCTLHPGAACAFGICCKDKCF 60
Db 399 PYPGNIFRLKYCGNLVVEEGECDCGTIRQCAKDPCCLLNCTLHPGAACAFGICCKDKCF 458
QY 61 LPSGTLCRQOVGECDLPEWNCSTSHQCPDDVVVDGISCNVNAFCYEKTCNNHDIQCKEI 120
Db 459 LPSGTLCRQOVGECDLPEWNCSTSHQCPDDVVVDGISCNVNAFCYEKTCNNHDIQCKEI 518
QY 121 FQDARSASQSCYQBIINTQGNRFGHCGIVGTTVVKWTPDIMCGRVQCNVGVIPNLIEH 180
Db 519 FQDARSASQSCYQBIINTQGNRFGHCGIVGTTVVKWTPDIMCGRVQCNVGVIPNLIEH 578
QY 181 STVQOFHLNDTTCWGTDYHLGMAI 204
Db 579 STVQOFHLNDTTCWGTDYHLGMAI 602
RESULT 3
ADC78877
ID ADC78877 standard; protein; 726 AA.
XX AC ADC78877;
XX DT 01-JAN-2004 (first entry)
XX DE Human PRO protein #53.
XX KW human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
XX KV Crohn's disease.
XX OS Homo sapiens.
XX PN WO2003034984-A2.
XX PD 01-MAY-2003.
XX PF 15-OCT-2002; 2002WO-US033070.
XX PR 19-OCT-2001; 2001US-0340083P.
XX PA (GETH ) GENENTECH INC.
XX PI Goddard A, Gurney AL;
XX WPI; 2003-481990/45.
XX DR N-PSDB; ADC78876.
XX PT New PRO polynucleotide and polypeptide, useful for the manufacture of a
XX medicament for diagnosing or treating cancer or inflammatory bowel
XX disorder e.g., ulcerative colitis or Crohn's disease.
XX PS Claim 12; SEQ ID NO 106; 327pp; English.
XX CC The invention comprises the amino acid and coding sequences of human PRO
XX proteins. The DNA and protein sequences of the invention are useful for
XX the diagnosis and treatment of cancer and inflammatory bowel disease
XX (e.g. ulcerative colitis or Crohn's disease). The present amino acid
XX sequence represents a human PRO protein of the invention.
XX SQ Sequence 726 AA;
Query Match 100.0%; Score 1192; DB 7; Length 726;
Best Local Similarity 100.0%; Pred. No. 8.4e-88;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PYPGNIFRLKYCGNLVVEEGECDCGTIRQCAKDPCCLLNCTLHPGAACAFGICCKDKCF 60
XX
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 27, 2004, 21:35:56 ; Search time 116 Seconds
(without alignments)
554.877 Million cell updates/sec

Title: US-10-633-202-2_COPY_399_602

Perfect score: 1192

Sequence: 1 PYPGNIFRLKYGCVLVEEG.....QPHLNDTTTCGFDYHLGMAI 204

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.25.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	753	63.2	763	11 Q811Q4	Q811Q4 mus musculus
2	718.5	60.3	761	11 Q8CDV3	Q8CDV3 mus musculus
3	664	55.7	702	11 Q8BMR5	Q8BMR5 mus musculus
4	664	55.7	714	11 Q8K4K0	Q8K4K0 mus musculus
5	660	55.4	697	11 Q8BMR4	Q8BMR4 mus musculus
6	590.5	49.5	790	4 Q8TBZ7	Q8TBZ7 homo sapien
7	575	48.2	873	13 Q42595	Q42595 xenopus lae
8	572	48.0	845	11 Q81072	Q81072 mus musculus
9	572	48.0	853	11 Q8OU94	Q8OU94 mus musculus
10	567	47.6	655	4 Q8NFM6	Q8NFM6 homo sapien
11	519.5	43.6	732	11 Q811Q3	Q811Q3 mus musculus
12	517.5	43.4	703	11 Q8C0V3	Q8C0V3 mus musculus
13	507.5	42.6	754	11 Q8CGQ1	Q8CGQ1 mus musculus
14	502.5	42.2	473	11 Q80815	Q80815 mus musculus
15	502.5	42.2	763	11 Q8CGQ2	Q8CGQ2 mus musculus
16	501.5	42.1	735	11 Q60473	Q60473 cavia porce

17	489.5	41.1	751	11 P70535	P70535 rattus norv
18	485.5	40.7	474	6 Q95LW7	Q95LW7 macaca fasc
19	476	39.9	730	6 Q19051	Q19051 oryctolagus
20	472	39.6	706	13 Q42593	Q42593 xenopus lae
21	468.5	39.3	732	6 Q28484	Q28484 macaca fasc
22	467.5	39.2	713	6 Q28485	Q28485 macaca fasc
23	466.5	39.1	792	6 Q19061	Q19061 saguinus oe
24	466.5	39.1	919	6 Q28659	Q28659 oryctolagus
25	464	38.9	825	6 Q28477	Q28477 macaca fasc
26	464	38.9	838	6 Q19056	Q19056 papio anubi
27	464	38.9	905	6 Q28476	Q28476 macaca fasc
28	463.5	38.9	825	6 Q46652	Q46652 papio anubi
29	459.5	38.5	731	6 Q19050	Q19050 oryctolagus
30	451.5	37.9	821	6 Q19060	Q19060 saguinus oe
31	450	37.8	812	6 Q77779	Q77779 bos taurus
32	448	37.6	836	6 Q19057	Q19057 pongo pygma
33	444	37.2	804	11 Q60410	Q60410 cavia porce
34	440	36.9	203	11 P97777	P97777 rattus norv
35	438.5	36.8	899	13 Q8UVF1	Q8UVF1 coturnix co
36	428	35.9	155	6 Q77634	Q77634 sus scrofa
37	427	35.8	914	13 Q12960	Q12960 xenopus lae
38	426	35.7	735	6 Q866A8	Q866A8 sus scrofa
39	422.5	35.4	812	4 Q8N0W6	Q8N0W6 homo sapien
40	420	35.2	155	6 Q77635	Q77635 bos taurus
41	418	35.1	1023	5 Q967H9	Q967H9 strongyloce
42	413	34.6	922	13 Q8UVF2	Q8UVF2 coturnix co
43	407.5	34.2	694	5 Q9GZ15	Q9GZ15 drosophila
44	407.5	34.2	1182	5 Q9VKL1	Q9VKL1 drosophila
45	402.5	33.8	756	6 Q28483	Q28483 macaca fasc

ALIGNMENTS

RESULT 1

Q811Q4 ID Q811Q4 PRELIMINARY; PRT; 763 AA.
AC Q811Q4;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE ADAM29.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Testis;
RA Choi I., Cho C.;
RT "Cloning and characterization of ADAM29";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY190759; AAC38663.1; -
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006586; ADAM cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR001590; Peptidase M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR Pfam; PF00200; disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR ProDom; PD000564; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS00215; ADAM_MEPRO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS00214; DISINTEGRIN_2; 1.
SQ SEQUENCE 763 AA; 86444 MW; F9EF082C3BFBA80 CRC64;

Query Match 63.2%; Score 753; DB 11; Length 763;
Best Local Similarity 58.6%; Pred. No. 5e-72;

Matches 119; Conservative 41; Mismatches 43; Indels 0; Gaps 0;

```
QY 2 YPGNIFRLKYCGNLVVEGEECDGCTIROCAKDPCLLNCITLHPGAACAFAFGICCKCKFL 61
Db 396 YTKDIFDTRCGNGVVEKEQCDGSLRNCITNDLCMSNCTLTSGSSCAFLGCKCKCQFL 455
QY 62 PSGLTLCRQGVGCDLPWCNCGTSHOCPPDDVYVQDGI SCNVNAFCYEKTCNNHDIQCKEIF 121
Db 456 PSGLTLCRKNDNICLPWCNCGTSHGCPDDAYVEDGIPGVSAICYEKQCNDRNEHCRQIF 515
QY 122 GDARSASQCYOEINTQGNRFGHCGIVGTTVVKWCTPDIMCGRVQCNVGVIPNLIEHS 181
Db 516 GQNAKTASVHCYREINTRGDRGCHGCLQGTPYIKCKSNDALCGRIQCDNVVQIPNKKDHS 575
QY 182 TVQQPHLNDTTCWGTDYHLGMAI 204
Db 576 TIHFALVKNVSCWGTDTYHGTSL 598
```

RESULT 2

```
Q8CDV3 Q8CDV3 PRELIMINARY; PRT; 761 AA.
AC Q8CDV3;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE A disintegrin and metalloprotease domain 24.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK029528; BAC26497.1; -.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR ProDom; PD0006209; EGF like.
DR InterPro; IPR001590; Peptidase_M12B_N.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR Pfam; PF00200; disintegrin_1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50215; ADAM_MPEPO; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 761 AA; 85039 MW; 2184A903262A3683 CRC64;
```

Query Match 60.3%; Score 718.5; DB 11; Length 761;

Best Local Similarity 55.6%; Pred. No. 2.5e-68; Matches 114; Conservative 36; Mismatches 54; Indels 1; Gaps 1;

```
QY 1 PYPGNIFRLKYCGNLVVEGEECDGCTIROCAKDPCLLNCITLHPGAACAFAFGIC- KDCX 59
Db 398 PPSDIFQLKVCNGVIVEGEECDGSGSENCRNRCNCPSTLRSKAKCDTGLCCNRKQ 457
QY 60 FLPSGLTLCRQGVGCDLPWCNCGTSHOCPPDDVYVQDGI SCNVNAFCYEKTCNNHDIQCKE 119
Db 458 IQPSGLTLCRARENECDLPWCNCGTSHCPEDLFVQDGTSCPDGTYCYEKRCSNDSHVHQR 517
```

```
QY 120 IFGDARSASQCYOEINTQGNRFGHCGIVGTTVVKWCTPDIMCGRVQCNVGVIPNLIE 179
Db 518 VFGQLAMKASQCYKELNTRGDRFGNCGFINNEYVRCBSIDILCGRIQCDKRVGTLPILQ 577
QY 180 HSTVQQPHLNDTTCWGTDYHLGMAI 204
Db 578 HYTIHWFNSVSCWSTDYHLGMI 602
```

RESULT 3

```
Q8BMR5 Q8BMR5 PRELIMINARY; PRT; 702 AA.
AC Q8BMR5;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Similar to ADAM 26 precursor.
OS ADAM34.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK029590; BAC26524.1; -.
DR MGD; MGI:2181992; Adam34.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR Pfam; PF00200; disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR PRINTS; PR00289; Disintegrin.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50215; ADAM_MPEPO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 702 AA; 79278 MW; 31976863CA4CE0BE CRC64;
```

Query Match 55.7%; Score 664; DB 11; Length 702;

Best Local Similarity 54.4%; Pred. No. 1.6e-62; Matches 105; Conservative 33; Mismatches 55; Indels 0; Gaps 0;

```
QY 12 CGNLVVEGEECDGCTIROCAKDPCLLNCITLHPGAACAFAFGICCKDKFLPSGLTLCRQV 71
Db 398 CGNLVVEGEECDGSGSTESCLQDPCCSDCVLKPGAQCAFGICCKNCPFLKTGTVCBEK 457
QY 72 GECDLPEWNGTSHOCPPDDVYVQDGI SCNVNAFCYEKTCNNHDIQCKEIPGDARSASQS 131
Db 458 NECDLPEWNGTSHOCPPDDVYVQDGI SCNVNAFCYEKTCNNHDIQCKEIPGDARSADSI 517
QY 132 CYOEINTQGNRFGHCGIVGTTVVKWCTPDIMCGRVQCNVGVIPNLIEHSTVQQPHLNDT 191
Db 518 CIMENNRGDRFGNCGNDSSMTRRCNLADVLGRIQCNVITQLPQRNHETVHYTHFSNV 577
QY 192 TCWGTDYHLGMAI 204
||| ||||| |
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 27, 2004, 21:38:21 ; Search time 40 Seconds
(without alignments)
490.577 Million cell updates/sec

Title: US-10-633-202-2_COPY_399_602
Perfect score: 1152
Sequence: 1 PYPGNIFRLKYCGNLVVEEG.....QFHLNDTTCWGTVDYHLGMAI 204

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	567	47.6	655	JC7850	disintegrin and me
2	536.5	45.0	660	S71949	metalloproteinase
3	502.5	42.2	473	I42823	ADAM 4 protein pre
4	501.5	42.1	735	I48101	ADAM 6 protein pre
5	468.5	39.3	732	I52361	testicular metallo
6	467.5	39.2	713	I65253	disintegrin-like t
7	464	38.9	825	S55060	fertilin alpha-II
8	464	38.9	905	S55059	fertilin alpha-I
9	442	37.1	600	I49281	fertilin alpha pre
10	425.5	35.7	903	S60257	metrin alpha - mo
11	417.5	35.0	151	S60259	metrin gamma - mo
12	402.5	33.8	756	S47656	tMDC II protein -
13	401.5	33.7	814	G02390	disintegrin-like m
14	391.5	32.8	777	I48100	ADAM 5 protein pre
15	390	32.7	734	JC4861	fertilin beta cha
16	386.5	32.4	776	S28258	androgen-regulated
17	384	32.2	670	I65967	disintegrin-like m
18	375	31.5	735	G02937	fertilin beta - cr
19	374	31.4	789	S28259	androgen-regulated
20	372	31.2	571	S24789	jararagin C preu
21	371	31.1	609	S55270	catrocollastatin p
22	369	31.0	419	A59414	metalloproteinase
23	367	30.8	150	S60258	metrin beta - mou
24	359	30.1	429	A42972	coagulation factor
25	357.5	30.0	357	S23403	sperm surface prot
26	356.5	29.9	952	T18900	disintegrin and me
27	354	29.7	617	S48160	metalloproteinase
28	353	29.6	610	JC7530	vascular apoptosis
29	347	29.1	524	S38539	disintegrin-like m

30 345 28.9 1042 2 T26644
31 338 28.4 416 2 A37877
32 337 28.3 736 2 S47645
33 332.5 27.9 616 2 A55796
34 332 27.9 209 2 JX0266
35 329 27.6 216 2 JX0265
36 327.5 27.5 419 2 S41607
37 324 27.2 826 2 A60385
38 317 26.6 823 2 S18968
39 299.5 25.1 549 2 S48169
40 266 22.3 512 2 T37819
41 248 20.8 289 2 S23402
42 198.5 16.7 83 2 F35982
43 196 16.4 480 1 A30065
44 194.5 16.3 71 2 A33990
45 190 15.9 73 2 A23731

RESULT 1
JC7850
disintegrin and metalloproteinase(ADAM) 9 protein, short form - human
N:Alternate names: MDC9 protein; meltrin gamma
C:Species: Homo sapiens (man)
C:Date: 18-Nov-2002 #sequence_revision 18-Nov-2002 #text_change 31-Mar-2003
C:Accession: JC7850
R:Hotoda, N.; Koike, H.; Sasagawa, N.; Ishiura, S.
Biochem. Biophys. Res. Commun. 293, 800-805, 2002
A:Title: A secreted form of human ADAM9 has an alpha-secretase activity for APP.
A:Reference number: JC7850; MUID:22050095; PMID:12054541
A:Accession: JC7850
A:Molecule type: mRNA
A:Residues: 1-655 <HOT>
A:CROSS-references: GB:AF495383
C:Comment: This protein, which is a member of the a disintegrin and metalloprotease (AD: lular functions. It is proteolytically active, and has an alpha-secretase activity for C:Genetics:
A:Gene: adam9s

Query Match 47.6%; Score 567; DB 2; Length 655;
Best Local Similarity 46.4%; Pred. No. 1.8e-36;
Matches 97; Conservative 36; Mismatches 62; Indels 14; Gaps 4;

QY 1 PYPGNIFRLKYCGNLVVEEGECDCGTIRQCAKDPCL-LNCTLHPGACAFGICCKCK 59
406 KPDPDAYSAPOSGCNKLVDAEGECDCGTPKECELDPCCEGSTCKLKSFAECAYGDCCKDCR 465
QY 60 FLPSGTLCRQVQGECDLPEWNGTSHQCPDDVYVQDGI SC-VNNAFCVYEKTCNNHDIQCK 118
466 FLPGGTLCRGKTSCECDVEYCNSSQFCQPDVFIQNGYPCQNNKAYCYNGMCQYDAQCQ 525
QY 119 EIFGQDASASQSCVQIEINTQGNRFGHGVGTTVTKWTPDIMGRCVQCEVY-----G 172
DB 526 VIFGSKAAPKDCFIENSKGRFCNGFCGFSNGEYKCKATGNALCGKLCENVQIEPVRG 585
QY 173 VIPNLIEHSTVQQFHLNDTTCWGTVDYHLG 201
DB 586 IVPALIIQTPS-----RGTKCWGVDFQLG 608

RESULT 2
S71949
metalloproteinase 12 (EC 3.4.24.-) precursor - human
N:Alternate names: disintegrin 12; myeloma cell metalloproteinase MCMP
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 04-Feb-2000
C:Accession: S71949; PC4264
R:McKie, N.; Dallas, D.J.; Edwards, T.; Apperley, J.F.; Russell, R.G.G.; Croucher, P.I.
Biochem. J. 318, 459-462, 1996
A:Title: Cloning of a novel membrane-linked metalloproteinase from human myeloma cells.
A:Reference number: S71949; MUID:96404892; PMID:8809033

hypothetical prote
hemorrhagic protei
tMDC I protein - c
ecarin precursor -
platelet aggregati
atrolysin A (EC 3.
monocyte surface a
cyritestin precurs
metalloproteinase
probable zinc meta
sperm surface prot
bitan alpha - puff
trigramin precurs
aplaggin - easter
albolabrin - green

A;Accession: S71949
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-660 <MCK>
A;Experimental source: myeloma cells
R;McKie, N.; Edwards, T.; Dallas, D.J.; Houghton, A.; Stringer, B.; Graham, R.; Russell, B.; Biochem. Biophys. Res. Commun. 230, 335-339, 1997
A;Title: Expression of members of a novel membrane linked metalloproteinase family (ADAM)
A;Reference number: P04263; MUID:97168971; PMID:9016778
A;Accession: P04264
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-337 <MCF>
A;Experimental source: articular chondrocyte
C;Function:
A;Description: involved in cell/cell and cell/matrix interaction in a variety of cell types
A;Note: membrane-bound; belongs to reprolysin family of metalloproteinases
C;Superfamily: mouse meltrin alpha; disintegrin homology
C;Keywords: hydrolase; metalloproteinase; zinc
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-660/Product: pre-metalloproteinase 12 #status predicted <MAT>
F;54-59/Region: autoinhibitory
F;295-378/Domain: disintegrin homology <DIS>
F;574-598/Region: epidermal growth factor-like
F;622-642/Domain: transmembrane #status predicted <TM1>
F;57,229,233,239/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F;229,233,239/Binding site: zinc, catalytic (His) (active) #status predicted
F;230/Active site: Glu #status predicted

Query Match 45.0%; Score 536.5; DB 2; Length 660;
Best Local Similarity 38.5%; Pred. No. 4e-34;
Matches 97; Conservative 36; Mismatches 62; Indels 57; Gaps 5;

QY 1 PYPGNIFRLKYCGNLVWVEGECDCGTIRQCAKDPCCLLNCTLHPGAACAFCGCKCKX 59
Db 288 KPDEAYGAPSCGNKLVDAEGECDCGTPEKCELDPCCEGTCCKLKSFAECAYGDCCKDR 347

QY 60 FLPSGTLCRQVGECDLPWCNGTSHQCPDDVYVQDGISGVNNAFCYEKTCNNHDIQCK 118
Db 348 FLPGGTLCRGKTSECDVPEYCNQSQFCQPDVFIQNGYPCQNNKAYCYNGMCQYVDAQ 407

QY 119 BIFGQDARSASQCYOEINTQGNRFGHCGIVGTTVVKWT----- 158
Db 408 VIFGSKAAAPKDCFIENSKGDRFGNGCFSGNEVKKATGLSKFAPFLSTMLEAVR 467

QY 159 -----PDMCRVQCENV-----GVIPNLIHSTVQOQFHLN 189
Db 468 QTGTVLGSGVCCMSDCRIVTLVKNALCKQLQCENVQIPVPGVIPAIIQTPS-----R 521

QY 190 DTTCTGTDYHLG 201
Db 522 GTKCWGVDFQLG 533

RESULT 3
I49283
ADAM 4 protein precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 03-Nov-2000
R;Wolfsberg, T.G.; Straight, P.D.; Gerena, R.L.; Huovila, A.P.; Primakoff, P.; Myles, D.; Dev. Biol. 169, 378-383, 1995
A;Title: ADAM, a widely distributed and developmentally regulated gene family encoding m
A;Reference number: I48100; MUID:95269891; PMID:7750654
A;Accession: I49283
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-473 <RES>
A;Cross-references: EMBL:U22058; NID:g965013; PIDN:AAA74922.1; PID:g965014
C;Genetics:
A;Gene: ADAM4
C;Superfamily: mouse meltrin alpha; disintegrin homology
F;129-211/Domain: disintegrin homology <DIS>

Query Match 42.2%; Score 502.5; DB 2; Length 473;
Best Local Similarity 41.2%; Pred. No. 1.3e-31;
Matches 84; Conservative 36; Mismatches 71; Indels 7; Gaps 2;

QY 5 NIFRLKYCGNLVWVEGECDCGTIRQCAKDPCCLLNCTLHPGAACAFCGCKCKXFLPSG 64
Db 126 NMVEVPCGNKRVASEKDCGSKVKDCTTDAKCEVNCFTQGSACAAGCCLSKCFAPTG 185

QY 65 TLCRQVGECDLPWCNGTSHQCPDDVYVQDGISGVNNAFCYEKTCNNHDIQCKEIFQD 124
Db 186 TICTDKNGICDLPEYCSGASEHCPGNFYIMDGTGCPCLAVCTAGNCSDRHLQCCALFGYQ 245

QY 125 ARSASQSCYOEINTQGNRFGHCGI-----GVTVYKWTTPDIMCRVQCENVGVIPLNIEH 180
Db 246 VKGSPACYNELNVKGRFGNCGIIRGGSQPVPCQKDFVCGMIHCDGVSHIPGGGEH 305

QY 181 STVQOQFHLNDT---TCWGTDYHLG 201
Db 306 TTFYHLKVQDYKEEQCFGYDAHHG 329

RESULT 4
I48101
ADAM 6 protein precursor - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 31-Mar-2000
C;Accession: I48101
R;Wolfsberg, T.G.; Straight, P.D.; Gerena, R.L.; Huovila, A.P.; Primakoff, P.; Myles, D.; Dev. Biol. 169, 378-383, 1995
A;Title: ADAM, a widely distributed and developmentally regulated gene family encoding n
A;Reference number: I48100; MUID:95269891; PMID:7750654
A;Accession: I48101
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-735 <RES>
A;Cross-references: EMBL:U22061; NID:g965007; PIDN:AAA74919.1; PID:g965008
C;Genetics:
A;Gene: ADAM6
C;Superfamily: mouse meltrin alpha; disintegrin homology
F;404-486/Domain: disintegrin homology <DIS>

Query Match 42.1%; Score 501.5; DB 2; Length 735;
Best Local Similarity 44.5%; Pred. No. 2.2e-31;
Matches 85; Conservative 32; Mismatches 71; Indels 3; Gaps 2;

QY 11 YCGNLVWVEGECDCGTIRQCAKDPCCLLNCTLHPGAACAFCGCKCKFLPSGTLCRQ 70
Db 407 FCGNRIVDEGELDCGTGTCQVTPNCCQTCMFTAGSICDGDCCCTNCTYSPSGTLCRPI 466

QY 71 VGECDLPWCNGTSHQCPDDVYVQDGISGVNNAFCYEKTCNNHDIQCKEIFQDARSASQ 130
Db 467 RNICDLPEYCTGSQLTCPENLVMDGTPTCTEYGVCYQGNCSDLTTHCREIFGEKAMKGL 526

QY 131 SCYOEINTQGNRFGHCGIVGT--TVYKWTTPDIMCRVQCENVGVIPLNIEHSTVQOQFHL 188
Db 527 DCYQ-INLKNRFGHCRRRASQKSHIACATDVGGRQCNSVTHPLRLQEVSHQSKF 585

QY 189 NDTTCWGTDYH 199
Db 586 GNSWCFGVDEH 596

RESULT 5
I52361
testicular metalloproteinase-like, disintegrin-like, cysteine-rich protein IVa - crab-ea
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C;Accession: I52361
R;Perry, A.C.F.; Jones, R.; Hall, L.; Biochem. J. 312, 239-244, 1995
A;Title: Analysis of transcripts encoding novel members of the mammalian metalloprotease
active monkey tissues.

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 27, 2004, 21:35:21 ; Search time 24 Seconds
(without alignments)
442.596 Million cell updates/sec

Title: US-10-633-202-2_COPY_399_602
Perfect score: 1192
Sequence: 1 PYPGNIFRLKCYGNLVVEG.....QFHLNDTTCGTGYHLGMAI 204

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1192	100.0	726	1 AD20_HUMAN	O43506 homo sapien
2	864	72.5	722	1 AD21_HUMAN	Q9UKJ8 homo sapien
3	788	66.1	820	1 AD29_HUMAN	Q9UKF5 homo sapien
4	769	64.5	760	1 AD25_MOUSE	Q9R159 mus musculus
5	747	62.7	729	1 AD21_MOUSE	Q9J176 mus musculus
6	716.5	60.1	761	1 AD24_MOUSE	Q9J160 mus musculus
7	664	55.7	697	1 AD26_MOUSE	Q9R158 mus musculus
8	590.5	49.5	790	1 AD30_HUMAN	Q9UKF2 homo sapien
9	567	47.6	819	1 AD09_HUMAN	Q13443 homo sapien
10	461.5	38.7	789	1 AD01_RAT	P70505 rattus norv
11	450	37.8	791	1 AD1A_MOUSE	Q60813 mus musculus
12	442.5	37.1	909	1 AD12_HUMAN	Q43184 homo sapien
13	437.5	36.7	956	1 AD19_HUMAN	Q9R013 homo sapien
14	425.5	35.7	903	1 AD12_MOUSE	Q61824 mus musculus
15	425.5	35.7	920	1 AD19_MOUSE	Q35674 mus musculus
16	422.5	35.4	813	1 AD33_HUMAN	Q9B211 homo sapien
17	422	35.4	906	1 AD22_HUMAN	Q9P0K1 homo sapien
18	421	35.3	935	1 AD22_XENLA	O42596 xenopus lae
19	420	35.2	806	1 AD1B_MOUSE	Q8R534 mus musculus
20	418	35.1	745	1 AD02_BOVIN	O77780 bos taurus
21	418	35.1	857	1 AD22_MOUSE	Q9R1V6 mus musculus
22	401.5	33.7	814	1 AD15_HUMAN	Q13444 homo sapien
23	399.5	33.5	754	1 AD07_HUMAN	Q9H2U9 homo sapien
24	399.5	33.5	864	1 AD15_MOUSE	O88839 mus musculus
25	395	33.1	751	1 AD02_RABIT	Q28660 oryctolagus
26	390	32.7	735	1 AD02_HUMAN	Q99965 homo sapien
27	387	32.5	773	1 AD11_MOUSE	Q9R1V4 mus musculus
28	386.5	32.4	776	1 AD07_MACFA	Q28475 macaca fasc
29	386.5	32.4	797	1 AD33_MOUSE	Q923W9 mus musculus
30	385	32.3	452	1 AD11_XENLA	Q9P8Z3 xenopus lae
31	384	32.2	769	1 AD11_HUMAN	Q75078 homo sapien
32	380.5	31.9	816	1 AD15_RAT	Q9GYV0 r adam 15 p
33	377	31.6	788	1 AD07_MOUSE	O35227 mus musculus

RESULT 1
AD20_HUMAN
ID AD20_HUMAN STANDARD; PRT; 726 AA.
AC O43506; Q9UKJ9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE ADAM 20 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase domain 20).
GN ADAM20.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=98137801; PubMed=9469942;
RA Hooft van Hujsduijn R.;
RT "ADAM 20 and 21; two novel human testis-specific membrane metalloproteinases with similarity to fertilin-alpha.";
RL Gene 206:273-282 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99453762; PubMed=10524237;
RA Poindexter K., Nelson N., DuBoise R.F., Black R.A., Cerretti D.P.;
RT "The identification of seven metalloproteinase-disintegrin (ADAM) genes from genomic libraries.";
RL Gene 237:61-70 (1999).
CC -!- FUNCTION: May be involved in sperm maturation and/or fertilization.
CC -!- COFACTOR: Binds 1 zinc ion per subunit (Potential).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Testis specific.
CC -!- DOMAIN: A tripeptide motif (VGE) within disintegrin-like domain could be involved in the binding to egg integrin receptor and thus could mediate sperm/egg binding.
CC -!- DOMAIN: The cysteine-rich domain encodes putative cell-fusion peptides, which could be involved in sperm-egg fusion.
CC -!- PTM: Has no obvious cleavage site for furin endopeptidase, suggesting that the proteolytic processing is regulated.
CC -!- MISCELLANEOUS: May be the functional equivalent of ADAM 1/fertilin alpha which is a pseudogene in human.
CC -!- SIMILARITY: Belongs to peptidase family M12B.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 disintegrin domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; AF029899; AAC52041.1; -.

ALIGNMENTS

34	375	31.5	735	1 AD02_MACFA	Q28478 macaca fasc
35	375	31.5	776	1 AD28_MACFA	Q9X816 macaca fasc
36	374	31.4	789	1 AD07_RAT	Q63180 rattus norv
37	372	31.2	571	1 DISJ_BOTJA	P30431 bothrops ja
38	366	30.7	775	1 AD28_HUMAN	Q9UKQ2 homo sapien
39	359	30.1	735	1 AD02_MOUSE	Q60718 mus musculus
40	358	30.0	793	1 AD28_MOUSE	Q9J1N6 mus musculus
41	352	29.5	735	1 AD02_CAVPO	Q60411 cavia porce
42	349	29.3	737	1 AD02_RAT	Q63202 rattus norv
43	341	28.6	739	1 AD18_HUMAN	Q9V3Q7 homo sapien
44	338	28.4	416	1 HR1B_TRIFL	P20164 trimeresuru
45	333	27.9	746	1 AD18_MACFA	Q9S194 macaca fasc

```

DR EMBL; AF158643; AAD55254.1; -.
DR HSP; P18619; 1FVL.
DR MEROPS; M12.218; -.
DR Genew; HGNC:199; ADAM20.
DR MIM; 603712; -.
DR GO; GO:0008237; F:metallopeptidase activity; TAS.
DR GO; GO:0007338; P:fertilization (sensu Animalia); TAS.
DR InterPro; IPR006586; ADAM cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR Pfam; PF00200; disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS00215; ADAM_MEPRO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
DR PROSITE; PS00214; DISINTEGRIN_2; 1.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; FALSE_NEG.
KW Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
KW Transmembrane; EGF-like domain.
FT SIGNAL 1 31
FT PROPEP 32 206
FT CHAIN 207 726
FT DOMAIN 207 693
FT TRANSMEM 694 714
FT DOMAIN 715 726
FT DOMAIN 207 384
FT DOMAIN 407 493
FT DOMAIN 494 634
FT DOMAIN 635 663
FT SITE 173 173
FT SITE 469 471
FT ACT_SITE 343 343
FT METAL 342 342
FT METAL 346 346
FT METAL 352 352
FT DISULFID 357 379
FT DISULFID 465 478
FT DISULFID 635 646
FT DISULFID 640 652
FT DISULFID 654 663
FT CARBOHYD 191 191
FT CARBOHYD 226 226
FT CARBOHYD 378 378
FT CARBOHYD 438 438
FT CARBOHYD 479 487
FT CARBOHYD 587 587
FT CONFLICT 19 19
FT CONFLICT 109 109
FT CONFLICT 637 637
FT CONFLICT 726 726
FT CONFLICT 817 817
SQ SEQUENCE 726 AA; 81710 MW; BF356A671CD1C12 CRC64;

Query Match 100.0%; Score 1192; DB 1; Length 726;
Best Local Similarity 100.0%; Pred. No. 2.8e-90;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PYPGNIPLKYCGNLVWEGEGCDGTIRQCAKDPCCLLNCTLHPGAACAFGICCKCKF 60
DB 399 PYPGNIPLKYCGNLVWEGEGCDGTIRQCAKDPCCLLNCTLHPGAACAFGICCKCKF 458
QY 61 LPSGTLCRQQVGECDLPEWNCNGTSHQCDDVYVQDGI SCNVNAFCYKTKCNNHDIQCKEI 120

```

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	4030	100.0	2181	2	AA556461	Human SVP
2	4030	100.0	3230	8	ABZ76248	Human GEN
3	4004	99.4	2426	2	AA228636	Nucleotid
4	4004	99.4	2442	10	ADC78876	Human PRO
5	4004	99.4	2442	10	ADE95180	Farnesyl

XX New human SVPH1-26 DNA useful for the diagnosis and prognosis of
PT testicular cancers.
PT

PS Claim 1; Page 70-73; 96pp; English.

The present sequence encodes human SVPH1-26. Human SVPH1-26 polypeptides are proteinases implicated in fertilisation and spermatogenesis. They can be used as therapeutic agents. A proteinase inhibitor of the catalytic domain would inhibit SVPH1-26 activity and would be useful as a method for birth control. Also, an inhibitor of the disintegrin domain of SVPH1-26 may affect fertilisation. The proteinase activity of SVPH1-26 can also be used as a detergent additive for the removal of strains having a protein component. The SVPH1-26 polypeptides and fragments can also be used as molecular weight markers, as markers for determination of isoelectric points of sample proteins and as controls for establishing the extent of fragmentation of a protein sample. The products can also be used for identifying, separating or purifying cells that express SVPH1-26 polypeptides such as testis cells. They can be used for the diagnosis and prognosis of testicular cancers.

Sequence 2181 BP; 600 A; 423 C; 530 G; 628 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	218
Score:	4030.00	Matches:	726
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-10-633-202-2 (1-726) x AAX56461 (1-2181)

Qy	1	MetAlaValGlyGluProLeuValHisIleArgValThrLeuLeuLeuLeuTrpPheGly	20
Db	1	ATGGCAGTGGGTGAGCCCTGGTGACATCAAGGCTyTTCCTTCGTCTGCTCGCTGGCTTGGG	60
Qy	21	MetPheLeuSerIleSerGlyHisSerGlnAlaArgProSerGlnTyrPheThrSerPro	40
Db	61	ATGTTTTTGTCTATTCTTGGCCACCTCTCAGGCCAGGCCCTCCAGTATTTCATCTTCTCCA	120
Qy	41	GluValValIleProLeuLysValIleSerArgGlyArgGlyAlaLysAlaProGlyTrp	60
Db	121	GAAGTGGTGATCCCTTTGAAGTGATCAGCAGGGGCAGAGGTGCAAAAGGCTCTCGATGG	180
Qy	61	LeuSerTyrSerLeuArgPheGlyGlyGlnArgTyrIleValHisMetArgValAsnLys	80
Db	181	CTCTCTATAGCTGCGGTTTTGGGGGACAGAGATACATTGTGCCATCATGAGGGTAAATAAG	240
Qy	81	LeuLeuPheAlaAlaHisIleuProValPheThrTyrThrGluGlnHisAlaLeuLeuGln	100
Db	241	CTGTGTTGTGTGCACACCTTCTGTGTTCACTACACAGAGCAGCAGCCCTGCTCCAG	300
Qy	101	AspGlnProPheIleGlnAspCysTyrTyrHisGlyTyrValGluGlyValProGlu	120
Db	301	GATCAGCCCTTCATCCAGGATCACTGCTACTACCATGGTTATGTGGAGGGGGTCCCTGAG	360
Qy	121	SerLeuValAlaLeuSerThrCysSerGlyGlyPheLeuGlyMetLeuGlnIleAsnAsp	140
Db	361	TCCTTGGTTGGCCCTTAGTACCTGTTCTGGGGGCTTCTTGGAAATGCTACAGATAAATGAC	420
Qy	141	LeuValTyrGluIleLysProIleSerValSerAlaThrPheGluHisLeuValTyrLys	160
Db	421	CTTGTTTATGAATCAAGCCAATTAGTGTCTGCCACATTTGAAACCACTAGATATATAAG	480
Qy	161	IleAspSerAspAspThrGlnPheProMetArgCysGlyLeuThrGluGluLysIle	180
Db	481	ATAGACAGTGATGATACACAGTTTCCACCTATGAGATGTGGGTTAA CAGAAGAGAAATA	540
Qy	181	AlaHisGlnMetGluLeuGlnLeuSerTyrAsnPheThrLeuLysGlnSerSerPheVal	200
Db	541	GCACACCATGAGGTGCAATTGTCATATAATTTCACTCTGAAGCAAGATCTCTTTTGTG	600